

*T260X*

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Hiroyuki NAKANE, Chikara OHTO, Shinichi OHNUMA, Kazutake HIROOKA, Tokuzo NISHINO

(ii) TITLE OF INVENTION: Farnesyl Diphosphate Synthase

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Kenyon & Kenyon
- (B) STREET: One Broadway
- (C) CITY: New York
- (D) STATE: NY
- (E) COUNTRY: USA
- (F) ZIP: 10004

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3½ Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
- (D) SOFTWARE: WordPerfect 6.1 Windows

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: Not Yet Issued
- (B) FILING DATE: Concurrent Herewith
- (C) CLASSIFICATION: Not Yet Issued

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: JP 8-213211
- (B) FILING DATE: 24-JUL-96

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Edward W. Greason
- (B) REGISTRATION NUMBER: 18,918
- (C) REFERENCE/DOCKET NUMBER: 77670/495

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 425-7200
- (B) TELEFAX: (212) 425-5288

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

*24*

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Sulfolobus acidocaldarius
- (B) STRAIN: ATCC 33909

(ix) FEATURE:

- (A) KEY: Asp-rich domain
- (B) LOCATION: 82-86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ser Tyr Phe Asp Asn Tyr Phe Asn Glu Ile Val Asn Ser Val Asn  
5 10 15  
Asp Ile Ile Lys Ser Tyr Ile Ser Gly Asp Val Pro Lys Leu Tyr Glu  
20 25 30  
Ala Ser Tyr His Leu Phe Thr Ser Gly Gly Lys Arg Leu Arg Pro Leu  
35 40 45  
Ile Leu Thr Ile Ser Ser Asp Leu Phe Gly Gly Gln Arg Glu Arg Ala  
50 55 60  
Tyr Tyr Ala Gly Ala Ala Ile Glu Val Leu His Thr Phe Thr Leu Val  
65 70 75 80  
His Asp Asp Ile Met Asp Gln Asp Asn Ile Arg Arg Gly Leu Pro Thr  
85 90 95  
Val His Val Lys Tyr Gly Leu Pro Leu Ala Ile Leu Ala Gly Asp Leu  
100 105 110  
Leu His Ala Lys Ala Phe Gln Leu Leu Thr Gln Ala Leu Arg Gly Leu  
115 120 125  
Pro Ser Glu Thr Ile Ile Lys Ala Phe Asp Ile Phe Thr Arg Ser Ile  
130 135 140  
Ile Ile Ile Ser Glu Gly Gln Ala Val Asp Met Glu Phe Glu Asp Arg  
145 150 155 160  
Ile Asp Ile Lys Glu Gln Glu Tyr Leu Asp Met Ile Ser Arg Lys Thr  
165 170 175  
Ala Ala Leu Phe Ser Ala Ser Ser Ile Gly Ala Leu Ile Ala Gly  
180 185 190  
Ala Asn Asp Asn Asp Val Arg Leu Met Ser Asp Phe Gly Thr Asn Leu  
195 200 205  
Gly Ile Ala Phe Gln Ile Val Asp Asp Ile Leu Gly Leu Thr Ala Asp  
210 215 220  
Glu Lys Glu Leu Gly Lys Pro Val Phe Ser Asp Ile Arg Glu Gly Lys  
225 230 235 240  
  
Lys Thr Ile Leu Val Ile Lys Thr Leu Glu Leu Cys Lys Glu Asp Glu

245	250	255
Lys Lys Ile Val Leu Lys Ala Leu Gly Asn Lys Ser Ala Ser Lys Glu		
260	265	270
Glu Leu Met Ser Ser Ala Asp Ile Ile Lys Lys Tyr Ser Leu Asp Tyr		
275	280	285
Ala Tyr Asn Leu Ala Glu Lys Tyr Tyr Lys Asn Ala Ile Asp Ser Leu		
290	295	300
Asn Gln Val Ser Ser Lys Ser Asp Ile Pro Gly Lys Ala Leu Lys Tyr		
305	310	315
Leu Ala Glu Phe Thr Ile Arg Arg Arg Lys		
325	330	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sulfolobus acidocaldarius*
- (B) STRAIN: ATCC 33909

(ix) FEATURE:

- (A) KEY: Asp-rich domain coding
- (B) LOCATION: 246-258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGAGTTACT TTGACAACTA TTTTAATGAG ATTGTTAATT CTGTAAACGA CATTATTAAG	60
AGCTATATAT CTGGAGATGT TCCTAAACTA TATGAAGCCT CATATCATTT GTTTACATCT	120
GGAGGTAAGA GGTAAAGACC ATTAATCTTA ACTATATCAT CAGATTATT CGGAGGACAG	180
AGAGAAAGAG CTTATTATGC AGGTGCAGCT ATTGAAGTTC TTCATACTTT TACGCTTGTG	240
CATGATGATA TTATGGATCA AGATAATATC AGAAGAGGGT TACCCACAGT CCACGTGAAA	300
TACGGCTTAC CCTTAGCAAT ATTAGCTGGG GATTTACTAC ATGCAAAGGC TTTTCAGCTC	360
TTAACCCAGG CTCTTAGAGG TTTGCCAAGT GAAACCATAA TTAAGGCTTT CGATATTTC	420
ACTCGTTCAA TAATAATTAT ATCCGAAGGA CAGGCAGTAG ATATGGAATT TGAGGACAGA	480

28

ATTGATATAA AGGAGCAGGA ATACCTTGAC ATGATCTCAC GTAAGACAGC TGCATTATTC	540
TCGGCATCCT CAAGTATAGG CGCACTTATT GCTGGTGCTA ATGATAATGA TGTAAGACTG	600
ATGTCTGATT TCGGTACGAA TCTAGGTATT GCATTTCAGA TTGTTGACGA TATCTTAGGT	660
CTAACAGCAG ACGAAAAGGA ACTTGGAAAG CCTGTTTTA GTGATATTAG GGAGGGTAAA	720
AAGACTATAC TTGTAATAAA AACACTGGAG CTTTGTAAAG AGGACGAGAA GAAGATTGTC	780
CTAAAGGCGT TAGGTAATAA GTCAGCCTCA AAAGAAGAAT TAATGAGCTC AGCAGATATA	840
ATTAAGAAAT ACTCTTACA TTATGCATAC AATTTAGCAG AGAAATATTA TAAAAATGCT	900
ATAGACTCTT TAAATCAAGT CTCCTCTAAG AGTGATATAC CTGGAAAGGC TTTAAAATAT	960
CTAGCTGAAT TTACGATAAG AAGGAGAAAA TAA	993

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATACTTTT TCCTTGTGGC TGATGATATC ATGGATC

37

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CATACTTTT TCCTTGTGCT TGATGATATC ATGGATC

37

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CATACTTATT TCCTTGTGCT TGATGATATC ATGGATC

37

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:37
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATACTTATT TCCTTGTGGC TGATGATATC ATGGATC

37

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTTCTTCATA CTTATTGCT TATTCATGAT AGTATT

36

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATTCATGATG ATCTTCCATC GATGGATCAA GAT

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTTCCCTTG TGGCTGATGA TATCATG

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTTCCCTTG TGCTTGATGA TATCATG

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TATTCCTTG TGCTTGATGA TATCATG

27

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TATTCCTTG TGGCTGATGA TATCATG

27

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TATTCGCTTA TTCATGATGA TCTTCCATCG ATG

33

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

32

- (A) LENGTH: 27
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTACGCTTG TGCATGATGA TATTATG

27

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